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PATENT APPLICATION US/08/727, 084BCH CENTER 1600/2900 DATE: 10/30/98

14

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This Raw Listing contains the General Information Section and up to the first 5 pages.

SEQUENCE LISTING

5 pages. ENTERED

2 General Information: 3 (1)4 (i) APPLICANT: Pulst, Stefan M 5 6 7 (ii) TITLE OF INVENTION: NUCLEIC ACID ENCODING SPINOCEREBELLAR ATAXIA-2 AND PRODUCTS RELATED THERETO 8 9 10 (iii) NUMBER OF SEQUENCES: 19 11 (iv) CORRESPONDENCE ADDRESS: 12 13 (A) ADDRESSEE: Mueting, Raasch & Gebhardt, P.A. (B) STREET: 119 North Fourth Street 14 15 (C) CITY: Minneapolis 16 (D) STATE: Minnesota 17 (E) COUNTRY: USA (F) ZIP: 55401 18 19 (V) COMPUTER READABLE FORM: 20 21 (A) MEDIUM TYPE: Floppy disk 22 (B) COMPUTER: IBM PC compatible 23 (C) OPERATING SYSTEM: PC-DOS/MS-DOS (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 24 25 26 (vi) CURRENT APPLICATION DATA: (A) APPLICATION NUMBER: US 08/727,084 27 (B) FILING DATE: 08-OCT-1996 28 29 (C) CLASSIFICATION: 30 31 (viii) ATTORNEY/AGENT INFORMATION: 32 (A) NAME: Mueting, Ann M. 33 (B) REGISTRATION NUMBER: 33,977

(C) REFERENCE/DOCKET NUMBER: 232.00010101

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 612/305-1220

(B) TELEFAX: 612/305-1228

(2) INFORMATION FOR SEQ ID NO:1:

46

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 516 base pairs

(B) TYPE: nucleic acid

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PAGE: 2 RAW SEQUENCE LISTING PATENT APPLICATION US/08/727,084B

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(C) STRANDEDNESS: both (D) TOPOLOGY: both (ii) MOLECULE TYPE: DNA (genomic) (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1: 5.5 TTGGTAGCAA CGGAAACGGC GGCGGCGCGT TTCGGCCCGG CTCCCGGCGG CTCCTTGGTC TCGGCGGGCC TCCCCGCCC TTCGTCGTCG TCCTTCTCCC CCTCGCCAGC CCGGGCGCCC CTCCGCCGC GCCAACCCGC GCCTCCCCGC TCGGCGCCCG TGCGTCCCCG CCGCGTTCCG GCGTCTCCTT GGCGCCCC GCTCCCGGCT GTCCCCGCCC GGCGTGCGAG CCGGTGTATG GGCCCTCAC CATGTCGCTG AAGCCCCAGC AGCAGCAGCA GCAGCAGCAG CAACAGCAGC AGCAGCAACA GCAGCAGCAG CAGCAGCAGC AGCCGCCGCC CGCGGCTGCC AATGTCCGCA AGCCCGGCGG CAGCGGCCTT CTAGCGTCGC CCGCCGCCGC GCCTTCGCCG TCCTCGTCCT CGGTCTCCTC GTCCTCGGCC ACGGCTCCCT CCTCGGTGGT CGCGGCGACC TCCGGCGGCG GGAGGCCCGG CCTGGGCAGG TGGGTGTCGG CACCCC (2) INFORMATION FOR SEO ID NO:2: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 4481 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: both (D) TOPOLOGY: both (ii) MOLECULE TYPE: cDNA (ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION: 163..4101 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2: ACCCCGAGA AAGCAACCCA GCGCGCCGCC CGCTCCTCAC GTGTCCCTCC CGGCCCCGGG GCCACCTCAC GTTCTGCTTC CGTCTGACCC CTCCGACTTC CGGTAAAGAG TCCCTATCCG CACCTCCGCT CCCACCCGGC GCCTCGGCGC GCCCGCCCTC CG ATG CGC TCA GCG Met Arg Ser Ala

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	a aa		aam	aam	~~~	. am	~~~			~~~			mam				S29524.raw
100			GCT														222
101	_	ATa	Ala	PIO	Arg		Pro	АТа	vaı	Ата		GIU	Ser	Arg	Arg		
102	5					10					15					20	
103	000	~~	999		maa	~~~		maa	~~~	maa	ama	a. a	~~~	~~~	~~~		070
104			GCC														270
105	А⊥а	АТа	Ala	Arg		Pro	СТĀ	Trp	Arg		Leu	GIn	Arg	Pro		Arg	
106					25					30					35		
107							·										
108			GGG														318
109	Arg	ser	Gly	_	GTÀ	GTÄ	СТÀ	СТÄ		Ala	Pro	GTÀ	Pro	-	Pro	Ser	
110				40					45					50			
111																	
112			CCT														366
113	Ala	Ala	Pro	Pro	Pro	Pro	СТĀ		GTÀ	Pro	Pro	Pro		Arg	Gln	Ser	
114			55					60					65				
115																	
116			CCC														414
117	Ser		Pro	Ser	Ala	Ser	_ = =	Cys	Phe	Gly	Ser		Gly	Asn	Gly	Gly	
118		70					75					80					
119																	
120			TTT														462
121	_	Ala	Phe	Arg	Pro	_	Ser	Arg	Arg	Leu		GTÀ	Leu	Gly	Gly		
122	85					90					95					100	
123																	
124			CCC														510
125	Pro	Arg	Pro	Phe		vaı	vaı	Leu	Leu		Leu	Ala	Ser	Pro	_	Ala	
126					105					110					115		
127																	
128			GCC														558
129	Pro	Pro	Ата		Pro	Thr	Arg	АТа		Pro	Leu	СТĀ	Ата		Α⊥а	Ser,	
130				120					125					130			
131	~~~	~~~	~~~														
132			CGT														606
133	Pro	Pro	Arg	ser	СТА	vaı	ser		Ата	arg	Pro	АТА		стА	cys	Pro	
134			135					140					145				
135	000	000	000	шаа	a.a	000	аша	mam	000	000	ama	100	3 111/2	maa	аша		654
136			GCG														654
137 138	Arg	150	Ala	Cys	GIU	Pro		Tyr	GTA	Pro	Leu		мес	Ser	Leu	Lys	
139		130					155					160					
140	aaa	a a a	CAG	ara	ava	030	ana	aza	ava	C 3 3	030	ara	axa	a a a	C 3 3	asa	702
140			Gln														702
141	165	GIII	GIII	GIII	GIN	170	GIII	GIII	GIII	GIII	175	GIII	GIII	GIII	GIII	180	
142	103					170					1/3					100	
144	CAC	CAC	CAG	CAC	CAC	CAC	CAC	ccc	aaa	ccc	aaa	CCT	aaa	יחגג	CITIC	aaa	750
144																	/50
145	GIII	GTII	Gln	GTII	185	GTII	GTII	FIO	LIO	190	WTQ	ATG	HIG	HSII	195	AIG	
145					103					190					193		
147	አአጣ	aaa	GGC	aaa	אממ	aaa	Cmm	CITE N	ccc	maa.	aaa	aaa	CCC	aaa	COM	maa.	798
140			Cly														138
150	пур	FLU	оту	200	SET	сту	ьец	nea	205	Set	FIO	мта	WIG	210	FIO	PAT	
151				200					205					210			
152	מממ	ጥርር	TCG	TOO	TOO	QTP C	TOO	TO CO	TOO	maa.	aaa	N C C	G CIT	ccc	таа	mαα	846
134	CCG	100	100	100	TCG	GIC	100	106	100	T C G	GUU	ACG	CCT		100	TUG	045

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153	Pro	Ser	Ser	Ser	Ser	Val	Ser	Ser	Ser	Ser	Ala	Thr	Ala	Pro	Ser	Ser	
154			215					220					225				
155																	
156	GTG	GTC	GCG	GCG	ACC	TCC	GGC	GGC	GGG	AGG	CCC	GGC	CTG	GGC	AGA	GGT	894
157	Val	Val	Ala	Ala	Thr	Ser	Gly	Gly	Gly	Arg	Pro	Gly	Leu	Gly	Arg	Gly	
158		230					235					240					
159																	
160												ATT					942
161	Arg	Asn	Ser	Asn	Lys	Gly	Leu	Pro	Gln	Ser	Thr	Ile	Ser	Phe	Asp	Gly	
162	245					250					255					260	
163																	
164												ACA					990
165	Ile	Tyr	Ala	Asn	Met	Arg	Met	Val	His		Leu	Thr	Ser	Val		Gly	
166					265					270					275		
167																	
168												ATA					1038
169	Ser	Lys	Cys		Val	Gln	Val	Lys		Gly	Gly	Ile	Tyr		Gly	Val	
170				280					285					290			
171																	
172												CTT					1086
173	Phe	Lys		Tyr	Ser	Pro	Lys	-	Asp	Leu	Val	Leu	-	Ala	Ala	His	
174			295					300					305				
175																	
176												CGT					1134
177	GIU	_	Ser	Thr	GLU	ser		ser	GTÄ	Pro	гàг	Arg	GTu	GLU	тте	мет	
178		310					315					320					
179	a.a	3.00	3 000	mma	mma		mam	ma s	~~	mmm	amm	ama	cm.	a.a	mmm		1100
180 181												GTG					1182
182	325	Ser	TTE	Leu	FILE	330	cys	Ser	ASP	FIIE	335	Val	vaı	GTII	rne	340	
183	323					330					333					340	
184	САТ	አሞር	ĠAC	שככ	አ ርጥ	ጥለጥ	CCA	A A A	λGλ	CAT	CCT	ттт	አርጥ	GAC	ጥረጥ	CCT	1230
185												Phe					1230
186	nop	1100	nop	DCI	345	- 7 -	ALU	Dy S	AL 9	350	AIG	1110	****	rop	355	AIG	
187					010					550					333		
188	ATC	AGT	GCT	ΔΔΔ	GTG	ААТ	GGC	GAA	CAC	ΔΑΔ	GAG	AAG	GAC	СТС	GAG	ccc	1278
189												Lys					12,0
190				360			 1		365	1		-1-		370			
191																	
192	TGG	GAT	GCA	GGT	GAA	CTC	ACA	GCC	AAT	GAG	GAA	CTT	GAG	GCT	TTG	GAA	1326
193												Leu					
194		-	375					380					385				
195																	
196	AAT	GAC	GTA	TCT	AAT	GGA	TGG	GAT	CCC	AAT	GAT	ATG	TTT	CGA	TAT	AAT	1374
197	Asn	Asp	Val	Ser	Asn	Gly	Trp	Asp	Pro	Asn	Asp	Met	Phe	Arg	Tyr	Asn	
198		390				-	395	-			-	400		_	-		
199																	
200	GAA	GAA	AAT	TAT	GGT	GTA	GTG	TCT	ACG	TAT	GAT	AGC	AGT	TTA	TCT	TCG	1422
201	Glu	Glu	Asn	Tyr	Gly	Val	Val	Ser	Thr	Tyr	Asp	Ser	Ser	Leu	Ser	Ser	
202	405				_	410				-	415					420	
203																	
204												GAA					1470
205	Tyr	Thr	Val	Pro	Leu	Glu	Arg	Asp	Asn	Ser	Glu	Glu	Phe	Leu	Lys	Arg	

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														11	ı DI IT	SET: S2952	A raw
206					425					430				AI	435	JE1. J2732	4.14W
207										100					100		
208	GAA	GCA	AGG	GCA	AAC	CAG	TTA	GCA	GAA	GAA	ATT	GAG	TCA	AGT	GCC	CAG	1518
209	Glu	Ala	Arg	Ala	Asn	Gln	Leu	Ala	Glu	Glu	Ile	Glu	Ser	Ser	Ala	Gln	
210			Ū	440					445					450			
211																	
212	TAC	AAA	GCT	CGA	GTG	GCC	CTG	GAA	AAT	GAT	GAT	AGG	AGT	GAG	GAA	GAA	1566
213	Tyr	Lys	Ala	Arg	Val	Ala	Leu	Glu	Asn	Asp	Asp	Arg	Ser	Glu	Glu	Glu	
214			455					460					465				
215																	
216						CAG											1614
217	Lys	_	Thr	Ala	Val	Gln	_	Asn	Ser	Ser	Glu	Arg	Glu	Gly	His	Ser	
218		470					475					480					
219																	
220					_	AAT											1662
221		ASN	Thr	arg	GIU	Asn	гÀг	туг	тте	Pro		GTÀ	GIN	arg	ASN	_	
222	485					490					495					500	
223 224	CAR	аша	A ITI A	maa	maa	aa x	y Cim	000	202	030	8 8 00	ma s	000	a a m	х пт ст	aaa	1710
225						GGA Gly											1/10
225	GIU	Val	TTE	Ser	505	СТУ	Ser	GIY	Arg	510	ASII	ser	PIO	Arg	515	GIY	
227					303					310					313		
228	CAG	ССТ	GGA	TCG	GGC	TCC	ATG	CCA	TCA	AGA	TCC	ACT	тст	CAC	ACT	TCA	1758
229						Ser											
230			1	520	1				525	5				530			
231																	
232	GAT	TTC	AAC	CCG	AAT	TCT	GGT	TCA	GAC	CAA	AGA	GTA	GTT	AAT	GGA	GGT	1806
233	Asp	Phe	Asn	Pro	Asn	Ser	Gly	Ser	Asp	Gln	Arg	Val	Val	Asn	Gly	Gly	
234			535					540					545				
235																	
236						CCT											1854
237	Val		Trp	Pro	Ser	Pro	_	Pro	Ser	Pro	Ser		Arg	Pro	Pro	Ser	
238		550					555					560					
239	~~~		~~~			~~~		m.am	amm		a a m		~~`	~~~			1000
240						CCC											1902
241 242	565	Tyr	GIN	ser	сту	Pro	ASN	ser	Leu	Pro		Arg	Ата	Ата	Thr		
242	363					570					575					580	
243	ልሮል	caa	CCG	מממ	ጥሮሮ	AGG	מממ	ccc	ጥርር	caa	CCA	שרכ	λCλ	ccc	מממ	ጥረጥ	1950
245						Arg											1730
246		9	110	1.0	585	71.9		110	001	590		501	9		595	501	
247																	
248	CAC	CCC	TCT	GCT	CAT	GGT	TCT	CCA	GCT	CCT	GTC	TCT	ACT	ATG	CCT	AAA	1998
249						Gly											
250				600		-			605					610		=	
251																	
252						GGG											2046
253	Arg	Met	Ser	Ser	Glu	Gly	Pro		Arg	Met	Ser	Pro	Lys	Ala	Gln	Arg	
254			615					620					625				
255																	
256						AGA											2094
257	Hls		Arg	Asn	Hls	Arg		ser	ΑΙα	СŢУ	Arg	_	ser	тте	ser	ser	
258		630					635					640					

SEQUENCE VERIFICATION REPORT PATENT APPLICATION US/08/727,084B

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